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ISMAGS: Speeding Up Subgraph Enumeration using Dynamic Node Ordering and Symmetry Analysis

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ISMAGS

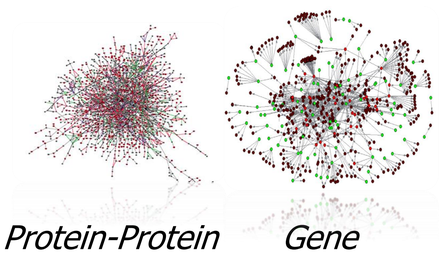
What is it?

The **I**ndex-based **S**ubgraph **M**atching **A**lgorithm with **G**eneral **S**ymmetries

- Subgraph enumeration algorithm
  - Finding all instances of a subgraph in a larger graph
    - Motif detection
    - Graphlet analysis
    - …

Where can we use it?

Biological networks



Protein-Protein Interaction — *Gene Regulatory*

General networks

Social Interaction — *Collaboration*

How does it work?

ISMAGS

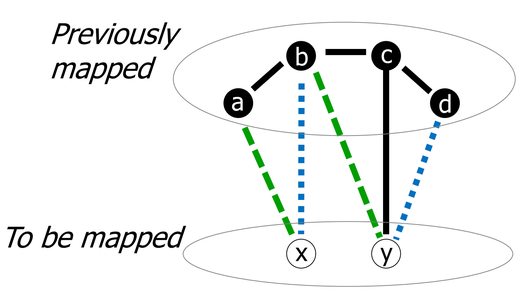
Exhaustive recursive search
Map each node of graph to node of subgraph & check for possible instance

Pruning search space

Dynamic Node Ordering | **Symmetry Analysis**

Dynamic Node Ordering

Optimised search space traversal during exhaustive search by determining best order of node mapping



- *Find subgraph instances by creating partial mappings*
- *Recursively expand partial mapping by selecting most constrained node*

Candidates for x =

$\cap$ {green neighbours of a}
{ blue neighbours of b}

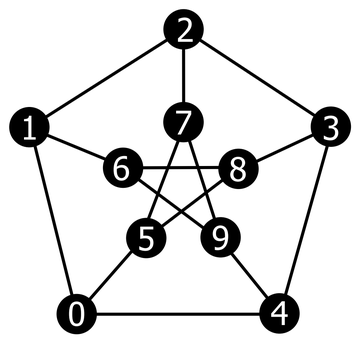
Candidates for y =

{green neighbours of b}
$\cap$ { black neighbours of c}
{ blue neighbours of d}

Limiting branching factor in search space

Symmetry Analysis

Customised symmetry analysis of the subgraph to avoid examining symmetric instances



1) *Determine generating permutations P*
2) *Extract stabiliser chains*
3) *Generate node index constraints C from coset representatives*

$$P = \left\{ \begin{matrix} (3\ 7)(4\ 5)(8\ 9) \\ (2\ 6)(3\ 8)(4\ 5)(7\ 9) \\ (1\ 4)(2\ 3)(6\ 9)(7\ 8) \\ (0\ 3\ 1\ 4\ 2)(5\ 8\ 6\ 9\ 7) \end{matrix} \right\}$$

$$C = \left\{ \begin{matrix} ID_0 < ID_1 & ID_0 < ID_6 & ID_1 < ID_4 \\ ID_0 < ID_2 & ID_0 < ID_7 & ID_1 < ID_5 \\ ID_0 < ID_3 & ID_0 < ID_8 & ID_2 < ID_6 \\ ID_0 < ID_4 & ID_0 < ID_9 & ID_3 < ID_7 \\ ID_0 < ID_5 & & \end{matrix} \right\}$$

Pruning search space by constraints

Results

Comparing ISMAGS to reference algorithms in a biological network (1.2K nodes) and a social network (7K nodes)

Network & subgraph	Time	Speedup factor per algorithm			
	ISMAGS	VF2	GK	G-Trie	ISMA
PPI network					
3-clique	8.81 ms	132.79	58.04	0.17	4.48
9-clique	92.21 ms	14509	41.36	7.28	4.68
Petersen	733.25 ms	9348	73.11	∞	451.25
Wikipedia elections					
3-clique	410.19 ms	456.35	68.12	0.22	4.37
Tetrahedron	320.72 ms	47.58	331.66	1.38	3.20
G4	448.54 ms	18.21	287.23	2.24	1.29

Improvement over VF2 & GK ?

- Optimised implementation of partial mapping generation and expansion

Improvement over G-Trie ?

- Dynamic node order reduces backtracking
  Better scaling: larger gains for larger subgraphs

Improvement over ISMA ?

- Symmetry constraints avoid exploring symmetric parts of search space

ISMAGS

Speeding up subgraph enumeration
Enabling larger graph analysis
Opening future research possibilities

M. Houbraken, S. Demeyer, T. Michoel, P. Audenaert, D. Colle, M. Pickavet (2014) The Index-Based Subgraph Matching Algorithm with General Symmetries (ISMAGS): Exploiting Symmetry for Faster Subgraph Enumeration, PLOS ONE (accepted).